

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/539,535
Source: PG/10
Date Processed by STIC: 6/27/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/539,535</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/539,535

DATE: 06/27/2005
TIME: 13:45:00

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272005\J539535.raw

use English in a
U.S. application

W--> 1 **SEQUENZPROTOKOLL** SEQUENCE LISTING

3 <110> APPLICANT: Ernst-Moritz-Arndt Universitat Greifswald

6 <120> TITLE OF INVENTION: Verwendung des multifunktionellen Transkriptionsfaktors Yin-

Yang-1

7 und Varianten davon zur Behandlung von Erkrankungen, insbesondere von Typ-1
8 Diabetes

10 <130> FILE REFERENCE: P 62096

C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/539,535

C--> 12 <141> CURRENT FILING DATE: 2005-06-17

12 <160> NUMBER OF SEQ ID NOS: 231

14 <170> SOFTWARE: PatentIn version 3.1

see item 4 on
Error summary
Does Not Comply
Specified Diskette Neede

ERRORED SEQUENCES

997 <210> SEQ ID NO: 13

998 <211> LENGTH: 21 24 shown

999 <212> TYPE: DNA

1000 <213> ORGANISM: Artificial

1002 <220> FEATURE:

1003 <223> OTHER INFORMATION: Synthetischer Oligonukleotidprimer

1005 <400> SEQUENCE: 13

E--> 1006 gtcttcgtcg tcgtcctcct cctc

24

use English (global err)

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

<210> 1
<211> 2256
<212> DNA
<213> Rattus norv.

<220>
<221> CDS
<222> (73)..(1125)
<223> YY1 (BB/OK)

<220>
<221> misc_feature
<222> (1759)..(1917)
<223> Zinkfinger Zinc finger

use
English

sample of English translation

Please correct globally.

10/539,535 3

<210> 32
<211> 21
<212> DNA
<213> Artificial

<400> 32
tcactggact tcaatttgcg c

<- needs explanation in <2207-223> section
(see p.5)

21

10/539,535 4

<210> 231
<211> 24
<212> DNA
<213> Artificial

(← needs explanation (see p. 5))

<400> 231
tctgagaggt caatgccagg tatac

24

71
1
delete

5

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/27/2005
PATENT APPLICATION: US/10/539,535 TIME: 13:45:01

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272005\J539535.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33
Seq#:34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57
Seq#:58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81
Seq#:82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104
Seq#:105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122
Seq#:123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140
Seq#:141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158
Seq#:159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176
Seq#:177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194
Seq#:195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212
Seq#:213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230
Seq#:231

Use of <220> Feature (NEW RULES):

error explanation

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:32,231

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/539,535

DATE: 06/27/2005
TIME: 13:45:01

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06272005\J539535.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:39
L:51 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:44
L:345 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:338
L:350 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:343
L:1006 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:24 SEQ:13
L:1231 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial
L:1231 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial
L:1231 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:1231
L:3624 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:231, <213>
ORGANISM:Artificial
L:3624 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:231, <213>
ORGANISM:Artificial
L:3624 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:231,Line#:3624